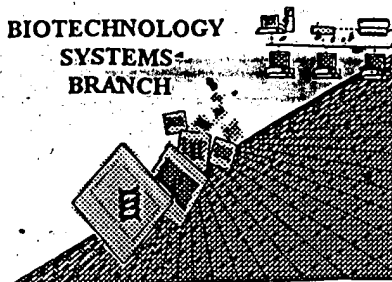


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/965536

Source: OIPE

Date Processed by STIC: 11/07/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/965536

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 3<sup>rd</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length.  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11      Use of <220>  
Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIKE

## RAW SEQUENCE LISTING

DATE: 11/07/2001

PATENT APPLICATION: US/09/965,536

TIME: 14:48:12

Input Set : A:\30534111.app

Output Set: N:\CRF3\11072001\I965536.raw

3 <110> APPLICANT: FEDER, J. N.  
 4 MINTIER, G.  
 5 RAMANATHAN, C. S.  
 6 HAWKEN, D. R.  
 8 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM5,  
 9 EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES  
 11 <130> FILE REFERENCE: DOO41NP/3053-4118US3  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/965,536 *OK*  
 14 <141> CURRENT FILING DATE: 2001-09-26  
 16 <150> PRIOR APPLICATION NUMBER: 60/235,713  
 17 <151> PRIOR FILING DATE: 2000-09-27  
 19 <150> PRIOR APPLICATION NUMBER: 60/261,781  
 20 <151> PRIOR FILING DATE: 2001-01-16  
 22 <150> PRIOR APPLICATION NUMBER: 60/306,605  
 23 <151> PRIOR FILING DATE: 2001-07-19  
 25 <150> PRIOR APPLICATION NUMBER: 60/310,436  
 26 <151> PRIOR FILING DATE: 2001-08-03  
 28 <160> NUMBER OF SEQ ID NOS: 61  
 30 <170> SOFTWARE: PatentIn Ver. 2.1  
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 40 tgcttaccctc gagctttttca ctgtgatggc aaggatgact gtgggaacgg ggcggacgaa 180  
 41 gagaactgtg gtgacactag tggatgggag accatatttg gcacagtga tggaaatgct 240  
 42 aacagcgtgg ccttaacaca ggagtgtttt ctaaaacagt atccacaatg ctgtgactgc 300  
 43 aaagaaactg aattggaatg tgtaaatggt gacttaaagt ctgtgccgat gattttctaac 360  
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 45 atcaaatata caaaacttaa aaagatatatt cttcagcata attgcattag acacatatcc 480  
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 57 atatgtatgc ccttgacgga cggcattttc tcatttgagg acctcttggc taacaatatc 1200  
 58 ctacagaatat ttgtctgggt tatagctttc attacctgct ttggaaatct tttgttcatt 1260  
 59 ggcattgagat ctttcattaa agctgaaaat acaactcacg ctatgtccat caaatcctt 1320  
 60 tgttgtgctg attgcctgat ggggtgtttac ttgttctttg ttggcatttt cgatataaaa 1380

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*for 221 and 222*

## RAW SEQUENCE LISTING

DATE: 11/07/2001

PATENT APPLICATION: US/09/965,536

TIME: 14:48:12

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Output Set: N:\CRF3\11072001\I965536.raw

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63 ttggagaagt tcctggatcat tgtcttcccc ttcagtaaca ttcgacctgg aaaacggcag 1560
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65 tggaataagg attatttttg aaacttttat gggaaaaatg gagtatgttt cccactttat 1680
66 tatgaccaa cagaagatat tggaagcaaa gggattcttc ttggaatttt cctaggtgtg 1740
67 aacttgctgg cttttctcat cattgtgttt tcctatatta ctatgttctg ttccattcaa 1800
68 aaaaccgcct tgcagaccac agaagtaagg aattgttttg gaagagaggt ggctgttgca 1860
69 aatcgtttct tttttatagt gttctctgat gccatctgct ggattcctgt attttagt 1920
70 aaaatccttt ccctcttccg ggtggaaata ccagacacaa tgacttcctg gatagtgatt 1980
71 tttttccttc cagttaacag tgctttgaat ccaatcctct atactctcac aaccaacttt 2040
72 ttttaaggaca agttgaaaca gctgctgcac aaacatcaga ggaaatcaat tttcaaaatt 2100
73 aaaaaaaaaa gtttatctac atccattgtg tggatagagg actcctcttc cctgaaactt 2160
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87 20 25 30
89 Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
90 35 40 45
92 Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
93 50 55 60
95 Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala
96 65 70 75 80
98 Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln
99 85 90 95
101 Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu
102 100 105 110
104 Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys
105 115 120 125
107 Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr
108 130 135 140
110 Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser
111 145 150 155 160
113 Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn
114 165 170 175
116 His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His
117 180 185 190
119 Gln Leu Thr Trp Leu Ile Leu Asp Asn Pro Ile Thr Arg Ile Ser
120 195 200 205
122 Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val
123 210 215 220
125 Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro
126 225 230 235 240

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## RAW SEQUENCE LISTING

DATE: 11/07/2001

PATENT APPLICATION: US/09/965,536

TIME: 14:48:12

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131 Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Phe Leu Pro
132           260           265           270
134 Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys
135           275           280           285
137 Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser
138           290           295           300
140 Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu Ser
141 305           310           315           320
143 Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu Lys
144           325           330           335
146 Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Asn
147           340           345           350
149 Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys
150           355           360           365
152 Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met Pro
153           370           375           380
155 Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn Ile
156 385           390           395           400
158 Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly Asn
159           405           410           415
161 Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr
162           420           425           430
164 His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met Gly
165           435           440           445
167 Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly Gln
168 450           455           460
170 Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser Val Gln Cys Arg Leu
171 465           470           475           480
173 Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu Leu
174           485           490           495
176 Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser
177           500           505           510
179 Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys Ile
180           515           520           525
182 Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro Phe Trp Asn Lys Asp
183           530           535           540
185 Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu Tyr
186 545           550           555           560
188 Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly Ile
189           565           570           575
191 Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser Tyr
192           580           585           590
194 Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu
195           595           600           605
197 Val Arg Asn Cys Phe Gly Arg Glu Val Ala Val Ala Asn Arg Phe Phe
198           610           615           620
200 Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/965,536

DATE: 11/07/2001

TIME: 14:48:12

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201 625          630          635          640
203 Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr Ser
204          645          650          655
206 Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile
207          660          665          670
209 Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu
210          675          680          685
212 Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser
213          690          695          700
215 Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu
216 705          710          715          720
218 Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro Val
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221 Ser
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241 agatgacatc tgcaatgctt ttcattctta ccaacggcaa gccttttctgc acagagagca 120
242 cagcagaatg gctcctgtca ctgcattcca atggcagctg tactatctac caaccgtgct 180
243 gaggacagca ccaaagggtc ctctcctcac cccacatgcc tgaaaagcac atgtgaattc 240
244 gtgtatagtg ggctgaggtg cagctgatct ctagctaata aacacaaccc accaacaagt 300
245 gaccacagtg tggcactgtg tggctcttca catcggggtg cactgtccat gaaatagaaa 360
246 cactcacaaat atctgattcc agtgtggcca taataacaga aatctaacaa ctctttcctt 420
247 gcctttttcaa tatcaaataa aaccatcagc atcctgctgg attgatagca aaggatttcc 480
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252 cttaaatatt cttaaagtat aatttcttta gacgagtatc cctattgctg gcaagttctg 780
253 ctttcataaa atatgcagat aagaagtgtt aaatgggatt caagaattat ggttttattt 840
254 gggactgttt gcatactcac aatgggtttg ttctcattgt ttttaacaaa aaagcaatga 900
255 agtttggggg ggttttttga aaacgaaact gaaaaaaatt atatgtgaaa atgagaactg 960
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257 aaaaag
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262 <212> TYPE: DNA
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## RAW SEQUENCE LISTING

DATE: 11/07/2001

PATENT APPLICATION: US/09/965,536

TIME: 14:48:12

Input Set : A:\30534111.app

Output Set: N:\CRF3\11072001\I965536.raw

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269 gagaactgtg gtgacactag tggatgggag accatatattg gcacagtgcg tggaaatgct 240
270 aacagcgtgg ccttaacaca ggagtgtttt ctaaaacagt atccacaatg ctgtgactgc 300
271 aaagaaactg aattggaatg tgtaaatggt gacttaaagt ctgtgccgat gattttctaac 360
272 aatgtgacat tactgtctct taagaaaaac aaaatccaca gtcttccaga taaagttttc 420
273 atcaaataca caaaacttaa aaagatatatt cttcagcata attgcattag acacatatcc 480
274 aggaaagcat tttttggatt atgtaatctg caaatattaa ttctagatga caatccaata 540
275 accagaatth cacagcgtct gtttacggga ttaaattcct tgtttttcct gtctatgggt 600
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278 tcgtcacacg tgctgtttct gcctagaaat caaattgggt ttgttccaga gaagacattt 780
279 tcttcattaa aaaatttagg agaactggat ctgtctagca atacgataac ggagctatca 840
280 cctcaccttt ttaaagactt gaagcttcta caaaagctga acctgtcatc caatcctctt 900
281 atgtatcttc acaagaacca gtttgaaagt cttaaacacac ttcatgtctc agacctggaa 960
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304 &lt;210&gt; SEQ ID NO: 6

305 &lt;211&gt; LENGTH: 713

306 &lt;212&gt; TYPE: PRT

307 &lt;213&gt; ORGANISM: Homo sapiens

309 &lt;400&gt; SEQUENCE: 6

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313 Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr
314             20             25             30
316 Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys
317             35             40             45
319 Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly
320             50             55             60
322 Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala

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097965536 6 of 7A

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<213> Artificial Sequence

<220>  
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N=A+G+C+T; K=C+G+T

<400> 29  
cgaagcgtaa gggcccagcc ggcnnknkn nnknknknkn nnknknknkn knknknknkn 60  
nnknknknkn nnknknknkn knkccgggt cgggcccgc 99

<210> 30  
<211> 95  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo 2;  
N=A+G+C+T; V=C+A+G

<400> 30  
aaaaggaaaa aagcggccgc vnnvnnvnnv nnvnnvnnv nnvnnvnnv vnnvnnvnnv 60  
nnvnnvnnv nnvnnvnnv gccgccgga ccgg 95

Does Not Comply  
Corrected Diskette Needed

Must enumerate unknowns "n's" in  
Fields 221, 222 and 223.

not

Fields 221 and 222 must be included in addition  
to Fields 223. Unknowns must be enumerated as  
follows: "unsure", some numeric location, and some  
possible value.

Notation is odd. Do you mean  
more clearly That N = A or G or C or T



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/965,536

DATE: 11/07/2001

TIME: 14:48:13

Input Set : A:\30534111.app

Output Set: N:\CRF3\11072001\I965536.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:1767 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29  
L:1767 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29  
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1768 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29  
L:1768 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29  
L:1768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
L:1781 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30  
L:1781 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30  
L:1781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1782 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30  
L:1782 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30  
L:1782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30